

## Figure 1

Amino Acid Sequence of EP01 (SEQ ID NO:1)

**F G K R E Q A E E E R Y F R A Q S R E Q L A A L**

The underlined section of the peptide corresponds to motif JJZX<sub>a</sub>Z<sub>b</sub>JX<sub>c</sub>JXJXJXZ

Amino Acid Sequence of EP02 (SEQ ID NO:4)

**G M D E L S E E D K L T V S R A R K I Q R F**

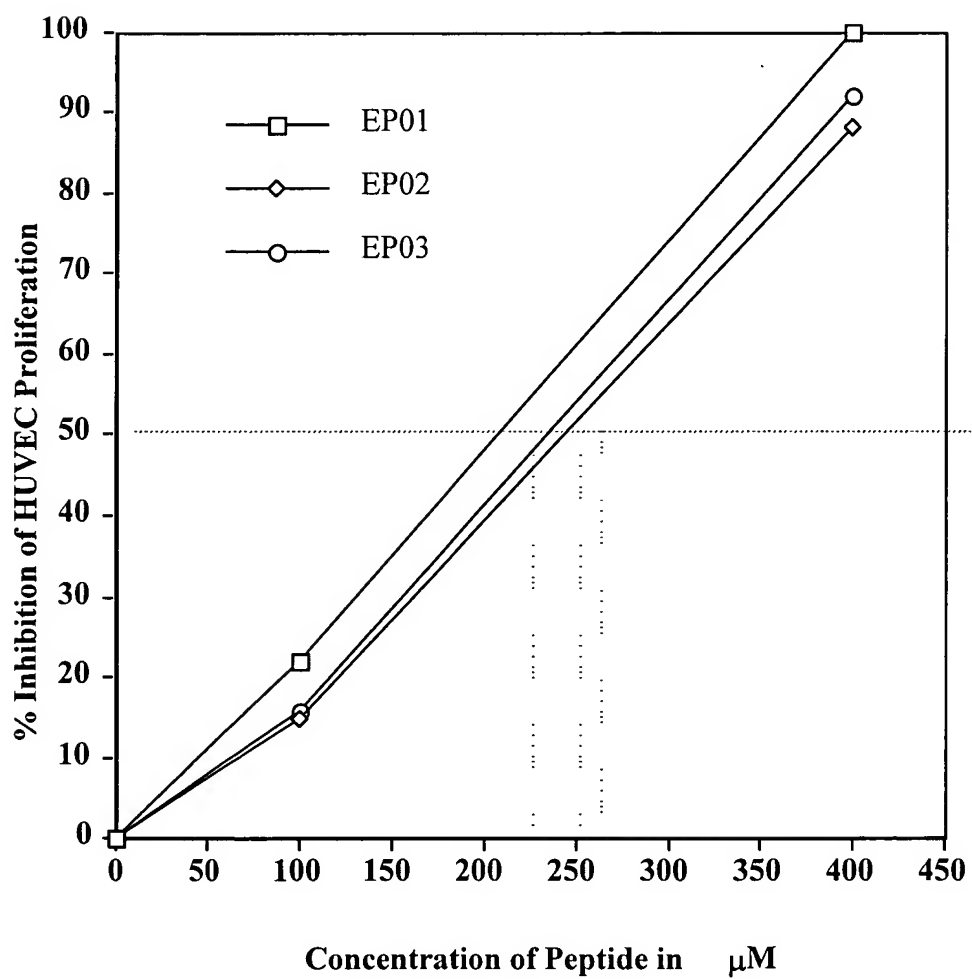
The underlined section of the peptide corresponds to motif ZZZJXXXXJXJJXXJ

Amino Acid Sequence of EP03 (SEQ ID NO:7)

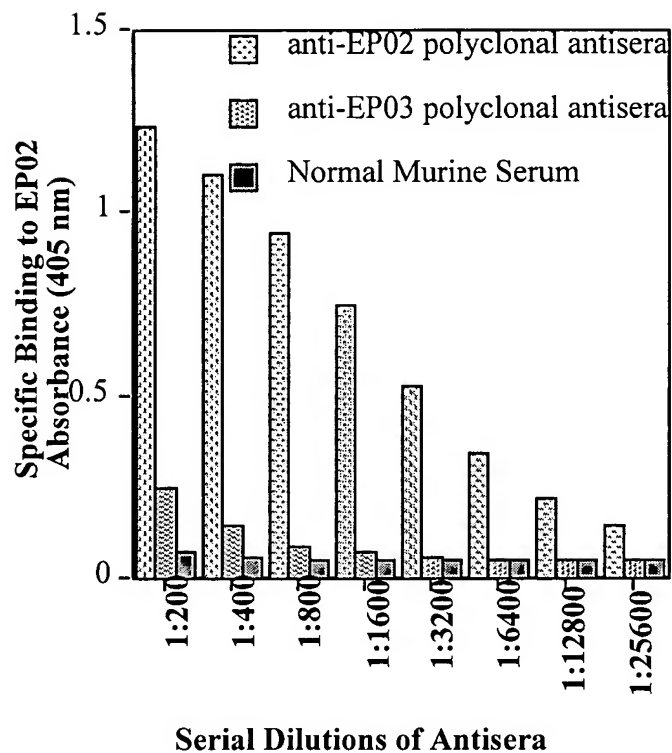
**S L Q D I I A I L G M D E L S E E D K L T C**

The underlined section of the peptide corresponds to motif ZZZJXXX

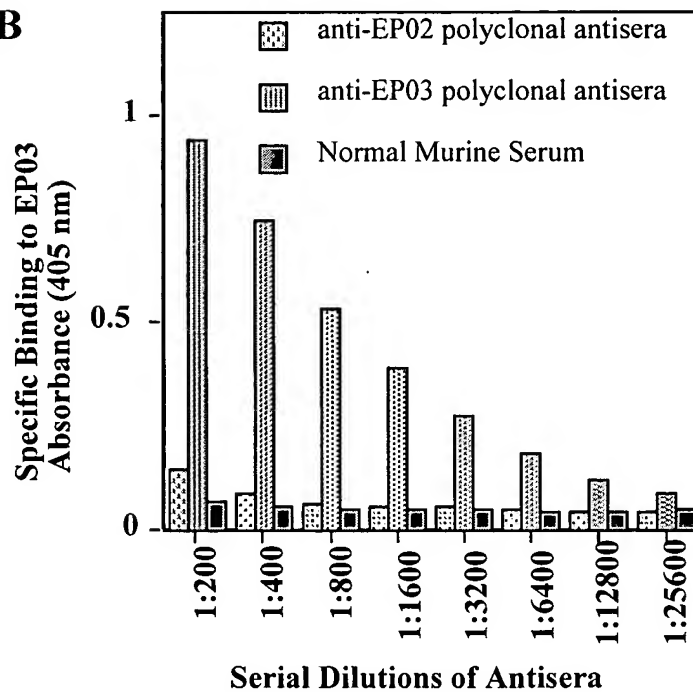
Figure 2



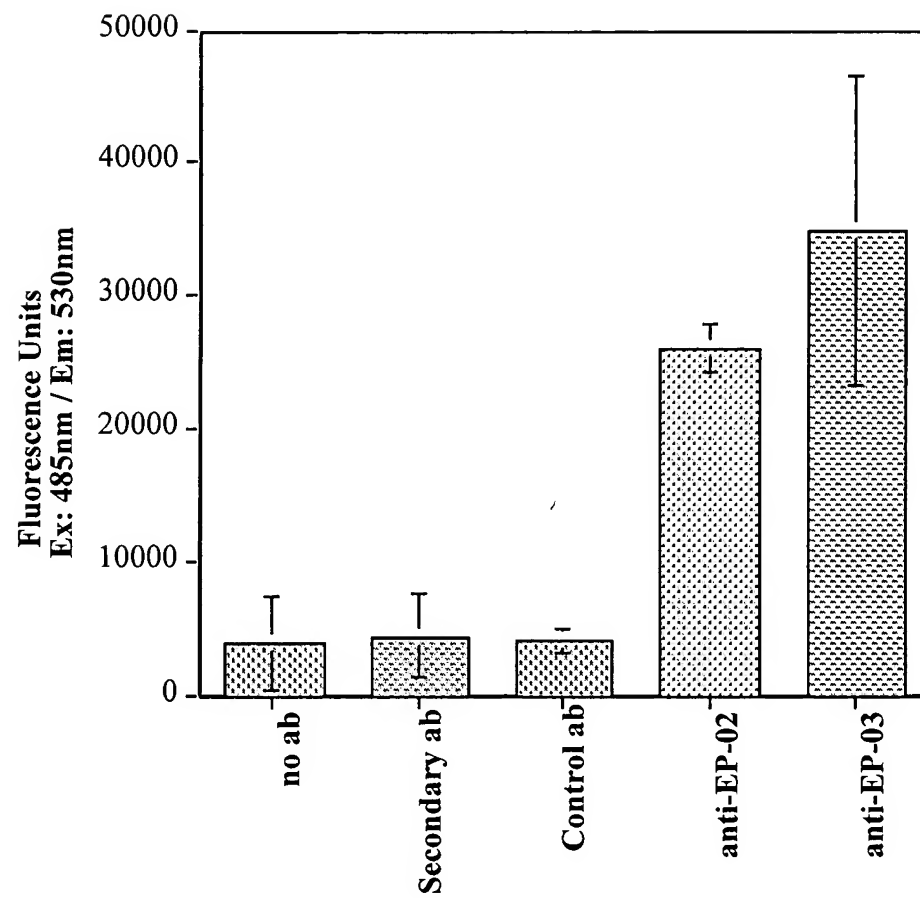
**Figure 3A**



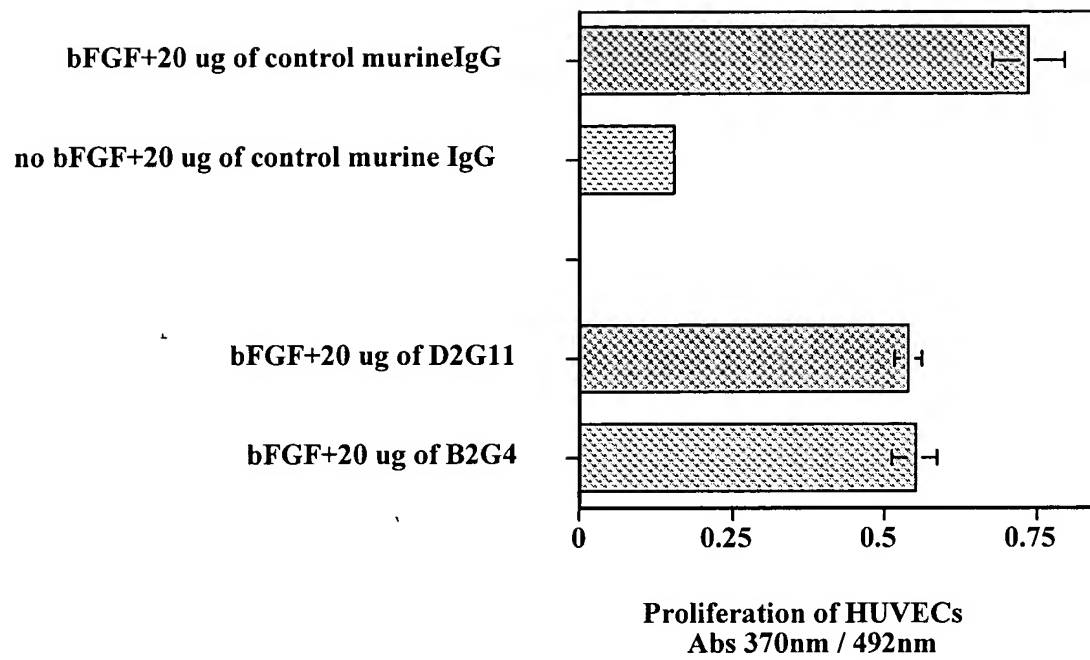
**Figure 3B**



**Figure 4**



**Figure 5**



## Figure 6

### DNA Sequence for V<sub>H</sub> (SEQ ID NO:8)

GAGGTGAASGTGGTGAATCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACT  
CTCCTGTGCAGCCTCTGGATTCACTTTCAGTAGCTATGCCATGTCTTGGGTTCGCCAGA  
CTCCAGAGAAGAGGCTGGAGTGGGTTCGCATCCATTAGTAGTGGTGGTAGCACCTACTAT  
CCAGACAGTGTGAAGGGCCGATTCACCATCTCCAGAGATAATGCCAGGAACATCCTGTA  
CCTGCAAATGAGCAGTCTGAGGTCTGAGGACACGGCCATGTATTACTGTGCAAGAGGCC  
TACCATTTGCTTACTGGGGCCAAGGACTCTGGTCACTGTCTCTGCAGAGAGTCAGTCC  
TTCCCAAATGTC

### Amino Acid Sequence for V<sub>H</sub> (SEQ ID NO:20)

10	20	30	40	50
EVXVVESGGG	LVKPGGSLKL	SCAASGFTFS	<u>SYAMSWVRQT</u>	PEKRLEWVAS
60	70	80	90	100
<u>ISSGGSTYYP</u>	<u>DSVKGRFTIS</u>	RDNARNILYL	QMSSLRSED	AMYYCARGLP
110	122			
<u>FAYWGQGLV</u>	TVSAESQSFP	NV		

## Figure 7

### DNA Sequence for V<sub>L</sub> (SEQ ID NO:9)

GATATTGTGATgACaCAATCTACAGCTTCCTTAGCTGTATCTCTGGGGCAGAGGGCCAC  
CATCTCATGCAGGGCCAGCCAAAGTGTCAGTACATCTAGCTATAGTTATATGCACTGGT  
ACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCAAGTATGCATCCAACCTAGAA  
TCTGGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACAT  
CCATCCTGTGGAGGAGGAGGATACTGCAACATATTACTGTCAGCACAGTTGGGAGATTC  
CGCTCACGTTTCGGTGCTGGGACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACT  
GTATCC

### Amino Acid Sequence for V<sub>L</sub> (SEQ ID NO:21)

10	20	30	40	50
DIVMTQSTAS	LAVSLGQRAT	<u>ISCRASQSVS</u>	<u>TSSYSYMHWY</u>	QQKPGQPPKL
60	70	80	90	100
LIKY <u>ASNLES</u>	GVPARFSGSG	SGTDFTLNIH	PVEEEDTATY	YCQHSWEIPL
110	120			
<u>TFGAGTKLEL</u>	KRADAAPTVS			